

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1.-16. (Cancelled)

17. (Currently Amended) A method of simultaneously detecting or quantifying n kinds of different target nucleic acids in a specimen, wherein each target nucleic acid contains a first ~~predetermined~~ partial sequence Fa and a second ~~predetermined~~ partial sequence Sa and each of the target nucleic acids is set forth as ~~(Fa, Sa)~~ Fa-Sa, wherein Fa is ~~[[any]]~~ one of ~~the first predetermined partial sequences F1 to Fn~~, and Sa is ~~[[any]]~~ one of ~~the second predetermined partial sequences S1 to Sn~~, wherein n is an integer of 2 or more comprising:

(a) preparing ~~probes Aa and Ba, wherein Aa is any one of the probes groups A1 to An and Ba is any one of the probes groups B1 to Bn, Aa is one of the probes A1 to An and Ba is one of the probes B1 to Bn~~, wherein n is an integer of 2 or more,

~~said probe Aa being one of the respective first probes each of which~~ has a sequence F'a complementary to the ~~respective first partial sequence Fa of the target nucleic acid (Fa, Sa)~~ Fa-Sa and a first binding molecule bound to the sequence F'a, wherein F'a is ~~[[any]]~~ one of ~~[[the]]~~ sequences F'1 to F'n and wherein n is an integer of 2 or more, and

~~said probe Ba being one of the respective second probes each of which~~ has a sequence S'a complementary to the ~~respective second partial sequence Sa of the target nucleic acid and a flag bound to the sequence S'a, wherein said flag comprises four units~~ sequences SD, D0_j, D1_k, and ED, each of SD, D0_j, D1_k, and ED having a desired sequence, and

~~linked in the form of SD+D0_j+D1_k+ED~~ SD-D0_j-D1_k-ED; wherein the flag sequences D0_j and D1_k are located between SD and ED and a sequence combination of [[the]] D0_j and D1_k [[as]] is set forth in ~~(D0_j, D1_k)~~ as D0_j-D1_k being assigned respectively to the each of the respective target nucleic acid (Fa, Sa);

and wherein SD and ED are each primer sequences, wherein S'a is [[any]] one of [[the]] sequences S'1 to S'n and wherein n is an integer of 2 or more, and wherein j and k are arbitrary natural numbers,

(b) ~~mixing each pair of probe Aa and probe Ba~~ the probes A1 to An and the probes B1 to Bn with ~~specimens~~ the specimen containing target nucleic acid (Fa, Sa), respectively, thereby hybridizing the first probe Aa with the respective first partial sequence Fa of the target nucleic acid Fa-Sa and simultaneously hybridizing the second probe Ba with the respective second partial sequence Sa of the target nucleic acid Fa-Sa;

(c) ligating the first probe Aa and the second probe Ba, both being hybridized with that are located on the target nucleic acid (Fa, Sa) Fa-Sa, thereby obtaining a probe having both said probe Aa and said probe Ba ~~Aa and Ba~~ as set forth in ~~(Aa+Ba)~~ as Aa-Ba;

(d) binding the first binding molecule[[s]] of said probe Aa to substances capable of being paired up ~~therewith~~ with the first binding molecule, thereby recovering the probe ~~(Aa+Ba)~~ Aa-Ba;

(e) ~~dissociating the flag-sequence (D0_j-D1_k)~~ D0_j-D1_k;

(f) ~~amplifying the flag-sequence (D0_j-D1_k)~~ D0_j-D1_k by polymerase chain reaction (PCR), wherein the PCR uses a primer to ~~which~~ labeled with a marker substance is ~~bound~~, and thereby obtaining ~~the flag-sequence (D0_j-D1_k) to which~~ D0_j-D1_k labeled with the marker substance is bound; and

(g) detecting or quantifying the marker substance of ~~the flag-sequence (D0_j-D1_k)~~ D0_j-D1_k labeled with the marker substance, thereby detecting or quantifying the target nucleic acid (Fa, Sa) in the specimen.

18. (Cancelled)

19. (Currently Amended) The method according to claim 17, wherein step (e) further comprises:

amplifying the dissociated ~~flag-sequence (D0_j-D1_k)~~ D0_j-D1_k by PCR,

wherein the PCR uses a primer to ~~which~~ labeled with a second binding molecule is ~~bound~~, and thereby obtains ~~the flag-sequence (D0_j-D1_k) to which~~ D0_j-D1_k labeled with the second binding molecule is bound, and

binding the second binding molecules of ~~the flag sequence (D0_j, D1_k)~~ D0_j-D1_k labeled with the second binding molecule to substances capable of being paired ~~up therewith,~~ with the second binding molecule, thereby recovering ~~the flag sequence (D0_j, D1_k)~~ D0_j-D1_k labeled with the second binding molecule.

20.-21. (Cancelled)

22. (Currently Amended) The method according to claim 17, wherein, in said step (d), said substances capable of being paired ~~[[up]]~~ with the first binding molecules ~~[[is]]~~ are immobilized on beads such that the probe (Aa, Ba) Aa-Ba is recovered by binding ~~the probe Aa-Ba~~ Aa-Ba to the beads via the first binding molecules.

23. (Previously Presented) The method according to claim 17, wherein said marker substance is a fluorescent substance such that the target nucleic acids are detected or quantified by quantifying the fluorescent substance.

24. (Cancelled)

25. (Currently Amended) The method according to claim 17, wherein ~~each of said flag sequences (D0_j, D1_k)~~ D0_j-D1_k is ~~[[a]]~~ double stranded sequence.

26.-33. (Cancelled)